

SEQUENCE LISTING

<110> AL MAHMOOD, SALMAN  
<120> Antisense oligonucleotides capable of inhibiting the formation of capillary tubes by endothelial cells  
<130> B6531-PCT-June 2002  
<140> PCT/FR02/xxxxxx  
<141> 2002-06-14  
<150> FR01/07805  
<151> 2001-06-14  
<160> 29  
<170> PatentIn version 3.1  
<210> 1  
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<223> Antisense oligonucleotide.
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23

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25

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tatccggagg gcctgccatg ctgct
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24

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23

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<400> 8  
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22

<210> 9  
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<223> Antisense oligonucleotide.

<400> 9  
tatccggagg gcctgccatg c

21

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<400> 10  
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20

<210> 11  
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<400> 11  
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19

<210> 12  
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<222> (1)..(18)  
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<400> 12  
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18

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<222> (1)..(17)  
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<400> 13  
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17

<210> 14  
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<400> 14  
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16

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<223> Antisense oligonucleotide.
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<210> 17
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<210> 18
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<221> misc_feature
<222> (1)..(12)
<223> Ologonucleotide anti-sens.
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<400> 18  
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<222> (1)..(22)  
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<400> 19  
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<210> 20  
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<400> 20  
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<400> 21  
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13

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<210> 23
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<400> 23
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12

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<210> 24
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<400> 24
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14

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<210> 25
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<221> misc_feature
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<223> Antisense oligonucleotide.
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<400> 25
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14

<210> 26  
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<222> (1)..(14)  
<223> Antisense oligonucleotide.

<400> 26  
ttttttttt ttcg 14

<210> 27  
<211> 326  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> misc\_feature  
<222> (1)..(326)  
<223> IRS-1 gene fragment coding for insulin receptor substrat

<400> 27  
gtgccgagct gagttcctta taagaattaa tcttaatttt gtatttttc ctgtaagaca 60  
ataggccatg ttaattaaac tgaagaagga tatatttggc tgggtgttt caaatgtcag 120  
cttaaaaattg gtaattgaat ggaagcaaaa ttataagaag agaaaaattaa agtcttccat 180  
tgcatgtatt gtaaacagaa ggagatgggt gattccttca attcaaaagc tctcttgga 240  
atgaacaatg tggcgtttg taaattctgg aaatgtctt ctattcataa taaactagat 300  
actgttgatc tttaaaaaaaa aaaaaa 326

<210> 28  
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<213> Homo sapiens  
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<221> CDS  
<222> (1022)..(4750)  
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<400> 28  
cggcggcgcg gtcggagggg gccggcgcg agagccagac gcccggctt gttttggttg 60

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gcggcagcgc	ctcccgagga	acaggcgtct	tccccgaacc	cttcccaaac	ctccccatc	180
ccctctcgcc	cttgtccct	cccctcctcc	ccagccgcct	ggagcgaggg	gcagggatga	240
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tctgcgactg	agctggtatt	tgggcggctg	gtggcggctg	ggacggttgg	gggggtggag	480
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gcccaaggat	attnaatttg	cctcggaaat	cgctgcttcc	agaggggaac	tcaggaggga	600
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gcctcccccgc	cgggcgtgaa	gchcccgaaa	actccggctg	ggctctctcc	tgggctcagc	840
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ccccccacccg	gttggggggc	ggagcctccc	tctgctcagc	gttgggtggtg	gcgggtggcag	1020
c atg gcg agc cct ccg gag agc gat ggc ttc tcg gac gtg cgc aag gtg						1069
Met Ala Ser Pro Pro Glu Ser Asp Gly Phe Ser Asp Val Arg Lys Val						
1	5	10	15			
ggc tac ctg cgc aaa ccc aag agc atg cac aaa cgc ttc ttc gta ctg						1117
Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu						
20	25	30				
cgc gcg gcc agc gag gct ggg ggc ccg gcg cgc ctc gag tac tac gag						1165
Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu						
35	40	45				
aac gag aag aag tgg cgg cac aag tcg agc gcc ccc aaa cgc tcg atc						1213
Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile						
50	55	60				
ccc ctt gag agc tgc ttc aac atc aac aag cgg gct gac tcc aag aac						1261
Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn						
65	70	75	80			
aag cac ctg gtg gct ctc tac acc cgg gac gag cac ttt gcc atc gcg						1309
Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala						

85	90	95	
gcg gac agc gag gcc gag caa gac agc tgg tac cag gct ctc cta cag Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln 100	105	110	1357
ctg cac aac cgt gct aag ggc cac cac gac gga gct gcg gcc ctc ggg Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Leu Gly 115	120	125	1405
gcg gga ggt ggt ggg ggc agc tgc agc ggc agc tcc ggc ctt ggt gag Ala Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu 130	135	140	1453
gct ggg gag gac ttg agc tac ggt gac gtg ccc cca gga ccc gca ttc Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe 145	150	155	1501
aaa gag gtc tgg caa gtg atc ctg aag ccc aag ggc ctg ggt cag aca Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr 165	170	175	1549
aag aac ctg att ggt atc tac cgc ctt tgc ctg acc agc aag acc atc Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile 180	185	190	1597
agc ttc gtg aag ctg aac tcg gag gca gcg gcc gtg gtg ctg cag ctg Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Val Val Leu Gln Leu 195	200	205	1645
atg aac atc agg cgc tgt ggc cac tcg gaa aac ttc ttc ttc atc gag Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu 210	215	220	1693
gtg ggc cgt tct gcc gtg acg ggg ccc ggg gag ttc tgg atg cag gtg Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val 225	230	235	1741
gat gac tct gtg gtg gcc cag aac atg cac gag acc atc ctg gag gcc Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala 245	250	255	1789
atg cgg gcc atg agt gat gag ttc cgc cct cgc agc aag agc cag tcc Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser 260	265	270	1837
tcg tcc aac tgc tct aac ccc atc agc gtc ccc ctg cgc cggt cac cat Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His 275	280	285	1885
ctc aac aat ccc ccg ccc agc cag gtg ggg ctg acc cgc cga tca cgc Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg 290	295	300	1933
act gag agc atc acc gcc acc tcc ccg gcc agc atg gtg ggc ggg aag			1981

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys			
305	310	315	320
cca ggc tcc ttc cgt gtc cgc gcc tcc agt gac ggc gaa ggc acc atg			2029
Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met			
325	330	335	
tcc cgc cca gcc tcg gtg gac ggc agc cct gtg agt ccc agc acc aac			2077
Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn			
340	345	350	
aga acc cac gcc cac cggt cat cggt ggc agc gcc cggt ctg cac ccc ccg			2125
Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro			
355	360	365	
ctc aac cac agc cgc tcc atc ccc atg ccgt gct tcc cgc tgc tcg cct			2173
Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro			
370	375	380	
tcg gcc acc agc ccgt agt ctg tcg tcc agt agc acc agt ggc cat			2221
Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Thr Ser Gly His			
385	390	395	400
ggc tcc acc tcg gat tgt ctc ttc cca cggt cga tct agt gct tcg gtg			2269
Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val			
405	410	415	
tct ggt tcc ccc agc gat ggc ggt ttc atc tcc tcg gat gag tat ggc			2317
Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly			
420	425	430	
tcc agt ccc tgc gat ttc cggt agt tcc ttc cgc agt gtc act ccgt gat			2365
Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp			
435	440	445	
tcc ctg ggc cac acc cca cca gcc cgc ggt gag gag gag cta agc aac			2413
Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Leu Ser Asn			
450	455	460	
tat atc tgc atg ggt ggc aag ggg ccc tcc acc ctg acc gcc ccc aac			2461
Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn			
465	470	475	480
ggc cac tac att ttg tct cgg ggt ggc aat ggc cac cgc tgc acc cca			2509
Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro			
485	490	495	
gga aca ggc ttg ggc acg agt cca gcc ttg gct ggg gat gaa gca gcc			2557
Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala			
500	505	510	
agt gct gca gat ctg gat aat cgg ttc cga aag aga act cac tcg gca			2605
Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala			
515	520	525	

ggc aca tcc cct acc att acc cac cag aag acc ccg tcc cag tcc tca Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser 530 535 540	2653
gtg gct tcc att gag gag tac aca gag atg atg cct gcc tac cca cca Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro 545 550 555 560	2701
gga ggt ggc agt gga ggc cga ctg ccg gga cac agg cac tcc gcc ttc Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe 565 570 575	2749
gtg ccc acc cgc tcc tac cca gag gag ggt ctg gaa atg cac ccc ttg Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu 580 585 590	2797
gag cgt cgg ggg ggg cac cac cgc cca gac agc tcc acc ctc cac acg Glu Arg Arg Gly Gly His His Arg Pro Asp Ser Ser Thr Leu His Thr 595 600 605	2845
gat gat ggc tac atg ccc atg tcc cca ggg gtg gcc cca gtg ccc agt Asp Asp Gly Tyr Met Pro Met Ser Pro Gly Val Ala Pro Val Pro Ser 610 615 620	2893
ggc cga aag ggc agt gga gac tat atg ccc atg agc ccc aag agc gta Gly Arg Lys Gly Ser Gly Asp Tyr Met Pro Met Ser Pro Lys Ser Val 625 630 635 640	2941
tct gcc cca cag cag atc atc aat ccc atc aga cgc cat ccc cag aga Ser Ala Pro Gln Gln Ile Ile Asn Pro Ile Arg Arg His Pro Gln Arg 645 650 655	2989
gtg gac ccc aat ggc tac atg atg tcc ccc agc ggt ggc tgc tct Val Asp Pro Asn Gly Tyr Met Met Ser Pro Ser Gly Gly Cys Ser 660 665 670	3037
cct gac att gga ggt ggc ccc agc agc agc agc agc agc aac gcc Pro Asp Ile Gly Gly Pro Ser Ser Ser Ser Ser Asn Ala 675 680 685	3085
gtc cct tcc ggg acc agc tat gga aag ctg tgg aca aac ggg gta ggg Val Pro Ser Gly Thr Ser Tyr Gly Lys Leu Trp Thr Asn Gly Val Gly 690 695 700	3133
ggc cac cac tct cat gtc ttg cct cac ccc aaa ccc cca gtg gag agc Gly His His Ser His Val Leu Pro His Pro Lys Pro Pro Val Glu Ser 705 710 715 720	3181
agc ggt ggt aag ctc tta cct tgc aca ggt gac tac atg aac atg tca Ser Gly Gly Lys Leu Leu Pro Cys Thr Gly Asp Tyr Met Asn Met Ser 725 730 735	3229
cca gtg ggg gac tcc aac acc agc agc ccc tcc gac tgc tac tac ggc Pro Val Gly Asp Ser Asn Thr Ser Ser Pro Ser Asp Cys Tyr Tyr Gly 740 745 750	3277

cct gag gac ccc cag cac aag cca gtc ctc tcc tac tac tca ttg cca Pro Glu Asp Pro Gln His Lys Pro Val Leu Ser Tyr Tyr Ser Leu Pro 755 760 765	3325
aga tcc ttt aag cac acc cag cgc ccc ggg gag ccg gag gag ggt gcc Arg Ser Phe Lys His Thr Gln Arg Pro Gly Glu Pro Glu Glu Gly Ala 770 775 780	3373
cgg cat cag cac ctc cgc ctt tcc act agc tct ggt cgc ctt ctc tat Arg His Gln His Leu Arg Leu Ser Thr Ser Ser Gly Arg Leu Leu Tyr 785 790 795 800	3421
gct gca aca gca gat gat tct tcc tct tcc acc agc agc gac agc ctg Ala Ala Thr Ala Asp Asp Ser Ser Ser Ser Thr Ser Ser Asp Ser Leu 805 810 815	3469
ggt ggg gga tac tgc ggg gct agg ctg gag ccc agc ctt cca cat ccc Gly Gly Gly Tyr Cys Gly Ala Arg Leu Glu Pro Ser Leu Pro His Pro 820 825 830	3517
cac cat cag gtt ctg cag ccc cat ctg cct cga aag gtg gac aca gct His His Gln Val Leu Gln Pro His Leu Pro Arg Lys Val Asp Thr Ala 835 840 845	3565
gct cag acc aat agc cgc ctg gcc cgg ccc acg agg ctg tcc ctg ggg Ala Gln Thr Asn Ser Arg Leu Ala Arg Pro Thr Arg Leu Ser Leu Gly 850 855 860	3613
gat ccc aag gcc agc acc tta cct cgg gcc cga gag cag cag cag cag Asp Pro Lys Ala Ser Thr Leu Pro Arg Ala Arg Glu Gln Gln Gln Gln 865 870 875 880	3661
cag cag ccc ttg ctg cac cct cca gag ccc aag agc ccg ggg gaa tat Gln Gln Pro Leu Leu His Pro Pro Glu Pro Lys Ser Pro Gly Glu Tyr 885 890 895	3709
gtc aat att gaa ttt ggg agt gat cag tct ggc tac ttg tct ggc ccg Val Asn Ile Glu Phe Gly Ser Asp Gln Ser Gly Tyr Leu Ser Gly Pro 900 905 910	3757
gtg gct ttc cac agc tca cct tct gtc agg tgt cca tcc cag ctc cag Val Ala Phe His Ser Ser Pro Ser Val Arg Cys Pro Ser Gln Leu Gln 915 920 925	3805
cca gct ccc aga gag gaa gag act ggc act gag gag tac atg aag atg Pro Ala Pro Arg Glu Glu Thr Gly Thr Glu Glu Tyr Met Lys Met 930 935 940	3853
gac ctg ggg ccg ggc cgg agg gca gcc tgg cag gag agc act ggg gtc Asp Leu Gly Pro Gly Arg Arg Ala Ala Trp Gln Glu Ser Thr Gly Val 945 950 955 960	3901
gag atg ggc aga ctg ggc cct gca cct ccc ggg gct gct agc att tgc Glu Met Gly Arg Leu Gly Pro Ala Pro Pro Gly Ala Ala Ser Ile Cys	3949

965	970	975	
agg cct acc cg <sup>g</sup> gca gt <sup>g</sup> ccc agc agc cg <sup>g</sup> ggt gac tac atg acc atg Arg Pro Thr Arg Ala Val Pro Ser Ser Arg Gly Asp Tyr Met Thr Met			3997
980	985	990	
cag atg agt tgt ccc cgt cag agc tac gt <sup>g</sup> gac acc tcg cca gct gcc Gln Met Ser Cys Pro Arg Gln Ser Tyr Val Asp Thr Ser Pro Ala Ala			4045
995	1000	1005	
cct gta agc tat gct gac atg cga aca ggc att gct gca gag gag Pro Val Ser Tyr Ala Asp Met Arg Thr Gly Ile Ala Ala Glu Glu			4090
1010	1015	1020	
gt <sup>g</sup> agc ctg ccc agg gcc acc atg gct gct gcc tcc tca tcc tca Val Ser Leu Pro Arg Ala Thr Met Ala Ala Ala Ser Ser Ser Ser			4135
1025	1030	1035	
gca gcc tct gct tcc ccg act ggg cct caa ggg gca gca gag ctg Ala Ala Ser Ala Ser Pro Thr Gly Pro Gln Gly Ala Ala Glu Leu			4180
1040	1045	1050	
gct gcc cac tcg tcc ctg ctg ggg ggc cca caa gga cct ggg ggc Ala Ala His Ser Ser Leu Leu Gly Gly Pro Gln Gly Pro Gly Gly			4225
1055	1060	1065	
atg agc gcc ttc acc cg <sup>g</sup> gt <sup>g</sup> aac ctc agt cct aac cgc aac cag Met Ser Ala Phe Thr Arg Val Asn Leu Ser Pro Asn Arg Asn Gln			4270
1070	1075	1080	
agt gcc aaa gt <sup>g</sup> atc cgt gca gac cca caa ggg tgc cgg cgg agg Ser Ala Lys Val Ile Arg Ala Asp Pro Gln Gly Cys Arg Arg Arg			4315
1085	1090	1095	
cat agc tcc gag act ttc tcc tca aca ccc agt gcc acc cgg gt <sup>g</sup> His Ser Ser Glu Thr Phe Ser Ser Thr Pro Ser Ala Thr Arg Val			4360
1100	1105	1110	
ggc aac aca gt <sup>g</sup> ccc ttt gga gc <sup>g</sup> ggg gca gca gta ggg ggc ggt Gly Asn Thr Val Pro Phe Gly Ala Gly Ala Ala Val Gly Gly Gly			4405
1115	1120	1125	
ggc ggt agc agc agc agc agc gag gat gt <sup>g</sup> aaa cgc cac agc tct Gly Gly Ser Ser Ser Ser Ser Glu Asp Val Lys Arg His Ser Ser			4450
1130	1135	1140	
gct tcc ttt gag aat gt <sup>g</sup> tgg ctg agg cct ggg gag ctt ggg gga Ala Ser Phe Glu Asn Val Trp Leu Arg Pro Gly Glu Leu Gly Gly			4495
1145	1150	1155	
gcc ccc aag gag cca gcc aaa ctg tgt ggg gct gct ggg ggt ttg Ala Pro Lys Glu Pro Ala Lys Leu Cys Gly Ala Ala Gly Gly Leu			4540
1160	1165	1170	
gag aat ggt ctt aac tac ata gac ctg gat ttg gtc aag gac ttc			4585

Glu	Asn	Gly	Leu	Asn	Tyr	Ile	Asp	Leu	Asp	Leu	Val	Lys	Asp	Phe	
1175						1180						1185			
aaa	cag	tgc	cct	cag	gag	tgc	acc	cct	gaa	ccg	cag	cct	ccc	cca	4630
Lys	Gln	Cys	Pro	Gln	Glu	Cys	Thr	Pro	Glu	Pro	Gln	Pro	Pro	Pro	
1190						1195						1200			
ccc	cca	ccc	cct	cat	caa	ccc	ctg	ggc	agc	ggt	gag	agc	agc	tcc	4675
Pro	Pro	Pro	Pro	His	Gln	Pro	Leu	Gly	Ser	Gly	Glu	Ser	Ser	Ser	
1205						1210						1215			
acc	cgc	cgc	tca	agt	gag	gat	tta	agc	gcc	tat	gcc	agc	atc	agt	4720
Thr	Arg	Arg	Ser	Ser	Glu	Asp	Leu	Ser	Ala	Tyr	Ala	Ser	Ile	Ser	
1220						1225						1230			
ttc	cag	aag	cag	cca	gag	gac	cgt	cag	tag	ctcaactgga	catcacagca				4770
Phe	Gln	Lys	Gln	Pro	Glu	Asp	Arg	Gln							
1235						1240									
aatatttcat	gattcacaac	taggacctca	tatcttcctc	atcagtagat	ggtacgatgc										4830
atccatttca	gtttgtttac	tttatccat	cctcaggatt	tcattgactg	aactgcacgt										4890
tctatattgt	gccaagcgaa	aaaaaaaaat	gcactgtgac	accagaataa	tgagtctgca										4950
taaacttcat	cttcaacctt	aaggacttag	ctggccacag	tgagctgatg	tgcccaccac										5010
cgtgtcatga	gagaatgggt	ttactctcaa	tgcattttca	agatacattt	catctgctgc										5070
tgaaaactgtg	tacgacaaag	catcattgta	aattatttca	tacaaaactg	ttcacgttgg										5130
gtggagagag	tattaaatat	ttaacatagg	tttgattta	tatgtgtaat	tttttaaatg										5190
aaaatgtaac	ttttcttaca	gcacatctt	ttttggatg	tgggatggag	gtatacaatg										5250
ttctgttgta	aagagtggag	caaatgctta	aaacaaggct	taaaagagta	gaatagggt										5310
tgatccttgt	tttaagattg	taattcagaa	aacataatat	aagaatcata	gtgccataga										5370
tggttctcaa	ttgtatagtt	atatttgctg	atactatctc	ttgtcatata	aacctgatgt										5430
tgagctgagt	tccttataag	aattaatctt	aattttgtat	ttttcctgt	aagacaatag										5490
gccatgttaa	ttaaactgaa	gaaggatata	tttggctggg	tgtttcaaa	tgtcagctta										5550
aaattggtaa	ttgaatggaa	gcaaaattat	aagaagagga	aattaaagtc	ttccattgca										5610
tgtattgtaa	acagaaggag	atgggtgatt	cttcaattc	aaaagctctc	tttggaatga										5670
acaatgtggg	cgtttgtaaa	ttctggaaat	gtctttctat	tcataataaa	ctagatactg										5730
ttgatctttt															5790
															5800

<210> 29  
 <211> 1242  
 <212> PRT  
 <213> Homo sapiens  
 <400> 29

Met	Ala	Ser	Pro	Pro	Glu	Ser	Asp	Gly	Phe	Ser	Asp	Val	Arg	Lys	Val
1					5					10				15	
Gly	Tyr	Leu	Arg	Lys	Pro	Lys	Ser	Met	His	Lys	Arg	Phe	Phe	Val	Leu
		20							25					30	
Arg	Ala	Ala	Ser	Glu	Ala	Gly	Gly	Pro	Ala	Arg	Leu	Glu	Tyr	Tyr	Glu
	35					40							45		
Asn	Glu	Lys	Lys	Trp	Arg	His	Lys	Ser	Ser	Ala	Pro	Lys	Arg	Ser	Ile
	50					55						60			
Pro	Leu	Glu	Ser	Cys	Phe	Asn	Ile	Asn	Lys	Arg	Ala	Asp	Ser	Lys	Asn
	65					70			75				80		
Lys	His	Leu	Val	Ala	Leu	Tyr	Thr	Arg	Asp	Glu	His	Phe	Ala	Ile	Ala
		85						90					95		
Ala	Asp	Ser	Glu	Ala	Glu	Gln	Asp	Ser	Trp	Tyr	Gln	Ala	Leu	Leu	Gln
		100						105					110		
Leu	His	Asn	Arg	Ala	Lys	Gly	His	His	Asp	Gly	Ala	Ala	Ala	Leu	Gly
		115					120					125			
Ala	Gly	Gly	Gly	Gly	Ser	Cys	Ser	Gly	Ser	Ser	Gly	Leu	Gly	Glu	
	130					135					140				
Ala	Gly	Glu	Asp	Leu	Ser	Tyr	Gly	Asp	Val	Pro	Pro	Gly	Pro	Ala	Phe
	145					150			155			160			
Lys	Glu	Val	Trp	Gln	Val	Ile	Leu	Lys	Pro	Lys	Gly	Leu	Gly	Gln	Thr
		165						170					175		
Lys	Asn	Leu	Ile	Gly	Ile	Tyr	Arg	Leu	Cys	Leu	Thr	Ser	Lys	Thr	Ile
		180						185				190			
Ser	Phe	Val	Lys	Leu	Asn	Ser	Glu	Ala	Ala	Ala	Val	Val	Leu	Gln	Leu
		195					200					205			
Met	Asn	Ile	Arg	Arg	Cys	Gly	His	Ser	Glu	Asn	Phe	Phe	Phe	Ile	Glu
		210					215				220				
Val	Gly	Arg	Ser	Ala	Val	Thr	Gly	Pro	Gly	Glu	Phe	Trp	Met	Gln	Val
	225						230			235			240		
Asp	Asp	Ser	Val	Val	Ala	Gln	Asn	Met	His	Glu	Thr	Ile	Leu	Glu	Ala
			245					250					255		

Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser  
260 265 270

Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His  
275 280 285

Leu Asn Asn Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg  
290 295 300

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys  
305 310 315 320

Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met  
325 330 335

Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn  
340 345 350

Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro  
355 360 365

Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro  
370 375 380

Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Ser Thr Ser Gly His  
385 390 395 400

Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val  
405 410 415

Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly  
420 425 430

Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp  
435 440 445

Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Leu Ser Asn  
450 455 460

Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn  
465 470 475 480

Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro  
485 490 495

Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala  
500 505 510

Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala  
515 520 525

Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser  
530 535 540

Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro  
545 550 555 560

Gly Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe  
565 570 575

Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu  
580 585 590

Glu Arg Arg Gly Gly His His Arg Pro Asp Ser Ser Thr Leu His Thr  
595 600 605

Asp Asp Gly Tyr Met Pro Met Ser Pro Gly Val Ala Pro Val Pro Ser  
610 615 620

Gly Arg Lys Gly Ser Gly Asp Tyr Met Pro Met Ser Pro Lys Ser Val  
625 630 635 640

Ser Ala Pro Gln Gln Ile Ile Asn Pro Ile Arg Arg His Pro Gln Arg  
645 650 655

Val Asp Pro Asn Gly Tyr Met Met Ser Pro Ser Gly Gly Cys Ser  
660 665 670

Pro Asp Ile Gly Gly Pro Ser Ser Ser Ser Ser Asn Ala  
675 680 685

Val Pro Ser Gly Thr Ser Tyr Gly Lys Leu Trp Thr Asn Gly Val Gly  
690 695 700

Gly His His Ser His Val Leu Pro His Pro Lys Pro Pro Val Glu Ser  
705 710 715 720

Ser Gly Gly Lys Leu Leu Pro Cys Thr Gly Asp Tyr Met Asn Met Ser  
725 730 735

Pro Val Gly Asp Ser Asn Thr Ser Ser Pro Ser Asp Cys Tyr Tyr Gly  
740 745 750

Pro Glu Asp Pro Gln His Lys Pro Val Leu Ser Tyr Tyr Ser Leu Pro  
755 760 765

Arg Ser Phe Lys His Thr Gln Arg Pro Gly Glu Pro Glu Glu Gly Ala  
770 775 780

Arg His Gln His Leu Arg Leu Ser Thr Ser Ser Gly Arg Leu Leu Tyr  
785 790 795 800

Ala Ala Thr Ala Asp Asp Ser Ser Ser Thr Ser Ser Asp Ser Leu  
805 810 815

Gly Gly Gly Tyr Cys Gly Ala Arg Leu Glu Pro Ser Leu Pro His Pro  
820 825 830

His His Gln Val Leu Gln Pro His Leu Pro Arg Lys Val Asp Thr Ala

835	840	845
Ala Gln Thr Asn Ser Arg Leu Ala Arg Pro Thr Arg Leu Ser Leu Gly 850	855	860
Asp Pro Lys Ala Ser Thr Leu Pro Arg Ala Arg Glu Gln Gln Gln 865	870	875
Gln Gln Pro Leu Leu His Pro Pro Glu Pro Lys Ser Pro Gly Glu Tyr 885	890	895
Val Asn Ile Glu Phe Gly Ser Asp Gln Ser Gly Tyr Leu Ser Gly Pro 900	905	910
Val Ala Phe His Ser Ser Pro Ser Val Arg Cys Pro Ser Gln Leu Gln 915	920	925
Pro Ala Pro Arg Glu Glu Glu Thr Gly Thr Glu Glu Tyr Met Lys Met 930	935	940
Asp Leu Gly Pro Gly Arg Arg Ala Ala Trp Gln Glu Ser Thr Gly Val 945	950	955
Glu Met Gly Arg Leu Gly Pro Ala Pro Pro Gly Ala Ala Ser Ile Cys 965	970	975
Arg Pro Thr Arg Ala Val Pro Ser Ser Arg Gly Asp Tyr Met Thr Met 980	985	990
Gln Met Ser Cys Pro Arg Gln Ser Tyr Val Asp Thr Ser Pro Ala Ala 995	1000	1005
Pro Val Ser Tyr Ala Asp Met Arg Thr Gly Ile Ala Ala Glu Glu 1010	1015	1020
Val Ser Leu Pro Arg Ala Thr Met Ala Ala Ala Ser Ser Ser Ser 1025	1030	1035
Ala Ala Ser Ala Ser Pro Thr Gly Pro Gln Gly Ala Ala Glu Leu 1040	1045	1050
Ala Ala His Ser Ser Leu Leu Gly Gly Pro Gln Gly Pro Gly Gly 1055	1060	1065
Met Ser Ala Phe Thr Arg Val Asn Leu Ser Pro Asn Arg Asn Gln 1070	1075	1080
Ser Ala Lys Val Ile Arg Ala Asp Pro Gln Gly Cys Arg Arg Arg 1085	1090	1095
His Ser Ser Glu Thr Phe Ser Ser Thr Pro Ser Ala Thr Arg Val 1100	1105	1110
Gly Asn Thr Val Pro Phe Gly Ala Gly Ala Ala Val Gly Gly Gly 1115	1120	1125

Gly Gly Ser Ser Ser Ser Glu Asp Val Lys Arg His Ser Ser  
1130 1135 1140

Ala Ser Phe Glu Asn Val Trp Leu Arg Pro Gly Glu Leu Gly Gly  
1145 1150 1155

Ala Pro Lys Glu Pro Ala Lys Leu Cys Gly Ala Ala Gly Gly Leu  
1160 1165 1170

Glu Asn Gly Leu Asn Tyr Ile Asp Leu Asp Leu Val Lys Asp Phe  
1175 1180 1185

Lys Gln Cys Pro Gln Glu Cys Thr Pro Glu Pro Gln Pro Pro Pro  
1190 1195 1200

Pro Pro Pro Pro His Gln Pro Leu Gly Ser Gly Glu Ser Ser Ser  
1205 1210 1215

Thr Arg Arg Ser Ser Glu Asp Leu Ser Ala Tyr Ala Ser Ile Ser  
1220 1225 1230

Phe Gln Lys Gln Pro Glu Asp Arg Gln  
1235 1240